RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/574,306
Source: IFWP
Date Processed by STIC: 03/13/2007

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IFWP

RAW SEQUENCE LISTING DATE: 03/13/2007
PATENT APPLICATION: **US/10/574,306** TIME: 08:29:13

Input Set : **A:\50458.002001.txt**
Output Set: **N:\CRF4\03132007\J574306.raw**

<110> APPLICANT: Korherr, Christian
<120> TITLE OF INVENTION: Medical Use of TBK-1 or of Inhibitors Thereof
<130> FILE REFERENCE: 50458/002001
<140> CURRENT APPLICATION NUMBER: US 10/574,306
<141> CURRENT FILING DATE: 2006-04-03
<150> PRIOR APPLICATION NUMBER: PCT/EP2004/010996
<151> PRIOR FILING DATE: 2004-10-01
<150> PRIOR APPLICATION NUMBER: US 60/508,100
<151> PRIOR FILING DATE: 2003-10-02
<160> NUMBER OF SEQ ID NOS: 10
<170> SOFTWARE: PatentIn version 3.3
<210> SEQ ID NO: 1
<211> LENGTH: 3031
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

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 84 cactggcaga cgcatgggca catcaagaag gcactcatcc gaaagacaga aatgtagaaa   1740
 86 aactacaagt cctgttaaat tgcatgacag agatttacta tcagttcaaa aaagacaaag   1800
 88 cagaacgtag attagcttat aatgaagaac aaatccacaa atttgataag caaaaactgt   1860
 90 attaccatgc cacaaaagct atgacgcact ttacagatga atgtgttaaa aagtatgagg   1920
 92 catttttgaa taagtcagaa gaatggataa gaaagatgct tcatcttagg aaacagttat   1980
 94 tatcgctgac taatcagtgt tttgatattg aagaagaagt atcaaaatat caagaatata   2040
 96 ctaatgagtt acaagaaact ctgcctcaga aaatgtttac agcttccagt ggaatcaaac   2100
 98 ataccatgac cccaatttat ccaagttcta acacattagt agaaatgact cttggtatga   2160
100 agaaattaaa ggaagagatg gaaggggtgg ttaaagaact tgctgaaaat aaccacattt   2220
102 tagaaaggtt tggctcttta accatggatg gtggccttcg caacgttgac tgtctttagc   2280
104 tttctaatag aagtttaaga aaagtttccg tttgcacaag aaaataacgc ttgggcatta   2340
106 aatgaatgcc tttatagata gtcacttgtt tctacaattc agtatttgat gtggtcgtgt   2400
108 aaatatgtac aatattgtaa atacataaaa aatatacaaa tttttggctg ctgtgaagat   2460
110 gtaattttat cttttaacat ttataattat atgaggaaat ttgacctcag tgatcacgag   2520
112 aagaaagcca tgaccgacca atatgttgac atactgatcc tctactctga gtggggctaa   2580
114 ataagttatt ttctctgacc gcctactgga aatattttta agtggaacca aaataggcat   2640
116 ccttacaaat caggaagact gacttgacac gtttgtaaat ggtagaacgg tggctactgt   2700
118 gagtggggag cagaaccgca ccactgttat actgggataa caatttttt gagaaggata   2760
120 aagtggcatt attttatttt acaaggtgcc cagatcccag ttatccttgt atccatgtaa   2820
122 tttcagatga attattaagc aaacatttta aagtgaattc attattaaaa actattcatt   2880
124 tttttccttt ggccataaat gtgtaattgt cattaaaatt ctaaggtcat ttcaactgtt   2940
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131 <210> SEQ ID NO: 2
132 <211> LENGTH: 729
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <400> SEQUENCE: 2
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142 Gln Gly Ala Thr Ala Asn Val Phe Arg Gly Arg His Lys Lys Thr Gly
143             20                  25                  30
146 Asp Leu Phe Ala Ile Lys Val Phe Asn Asn Ile Ser Phe Leu Arg Pro
147         35                  40                  45
150 Val Asp Val Gln Met Arg Glu Phe Glu Val Leu Lys Lys Leu Asn His
151     50                  55                  60
154 Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Thr Thr Arg
155 65                  70                  75                  80
158 His Lys Val Leu Ile Met Glu Phe Cys Pro Cys Gly Ser Leu Tyr Thr
159                 85                  90                  95
162 Val Leu Glu Glu Pro Ser Asn Ala Tyr Gly Leu Pro Glu Ser Glu Phe
163             100                 105                 110
166 Leu Ile Val Leu Arg Asp Val Val Gly Gly Met Asn His Leu Arg Glu
167         115                 120                 125
170 Asn Gly Ile Val His Arg Asp Ile Lys Pro Gly Asn Ile Met Arg Val
171     130                 135                 140
174 Ile Gly Glu Asp Gly Gln Ser Val Tyr Lys Leu Thr Asp Phe Gly Ala
175 145                 150                 155                 160
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```
178 Ala Arg Glu Leu Glu Asp Asp Glu Gln Phe Val Ser Leu Tyr Gly Thr
179                 165                 170                 175
182 Glu Glu Tyr Leu His Pro Asp Met Tyr Glu Arg Ala Val Leu Arg Lys
183             180                 185                 190
186 Asp His Gln Lys Lys Tyr Gly Ala Thr Val Asp Leu Trp Ser Ile Gly
187         195                 200                 205
190 Val Thr Phe Tyr His Ala Ala Thr Gly Ser Leu Pro Phe Arg Pro Phe
191     210                 215                 220
194 Glu Gly Pro Arg Arg Asn Lys Glu Val Met Tyr Lys Ile Ile Thr Gly
195 225                 230                 235                 240
198 Lys Pro Ser Gly Ala Ile Ser Gly Val Gln Lys Ala Glu Asn Gly Pro
199                 245                 250                 255
202 Ile Asp Trp Ser Gly Asp Met Pro Val Ser Cys Ser Leu Ser Arg Gly
203             260                 265                 270
206 Leu Gln Val Leu Leu Thr Pro Val Leu Ala Asn Ile Leu Glu Ala Asp
207         275                 280                 285
210 Gln Glu Lys Cys Trp Gly Phe Asp Gln Phe Phe Ala Glu Thr Ser Asp
211     290                 295                 300
214 Ile Leu His Arg Met Val Ile His Val Phe Ser Leu Gln Gln Met Thr
215 305                 310                 315                 320
218 Ala His Lys Ile Tyr Ile His Ser Tyr Asn Thr Ala Thr Ile Phe His
219                 325                 330                 335
222 Glu Leu Val Tyr Lys Gln Thr Lys Ile Ile Ser Ser Asn Gln Glu Leu
223             340                 345                 350
226 Ile Tyr Glu Gly Arg Arg Leu Val Leu Glu Pro Gly Arg Leu Ala Gln
227         355                 360                 365
230 His Phe Pro Lys Thr Thr Glu Glu Asn Pro Ile Phe Val Val Ser Arg
231     370                 375                 380
234 Glu Pro Leu Asn Thr Ile Gly Leu Ile Tyr Glu Lys Ile Ser Leu Pro
235 385                 390                 395                 400
238 Lys Val His Pro Arg Tyr Asp Leu Asp Gly Asp Ala Ser Met Ala Lys
239                 405                 410                 415
242 Ala Ile Thr Gly Val Val Cys Tyr Ala Cys Arg Ile Ala Ser Thr Leu
243             420                 425                 430
246 Leu Leu Tyr Gln Glu Leu Met Arg Lys Gly Ile Arg Trp Leu Ile Glu
247         435                 440                 445
250 Leu Ile Lys Asp Asp Tyr Asn Glu Thr Val His Lys Lys Thr Glu Val
251     450                 455                 460
254 Val Ile Thr Leu Asp Phe Cys Ile Arg Asn Ile Glu Lys Thr Val Lys
255 465                 470                 475                 480
258 Val Tyr Glu Lys Leu Met Lys Ile Asn Leu Glu Ala Ala Glu Leu Gly
259                 485                 490                 495
262 Glu Ile Ser Asp Ile His Thr Lys Leu Leu Arg Leu Ser Ser Ser Gln
263             500                 505                 510
266 Gly Thr Ile Glu Thr Ser Leu Gln Asp Ile Asp Ser Arg Leu Ser Pro
267         515                 520                 525
270 Gly Gly Ser Leu Ala Asp Ala Trp Ala His Gln Glu Gly Thr His Pro
271     530                 535                 540
274 Lys Asp Arg Asn Val Glu Lys Leu Gln Val Leu Leu Asn Cys Met Thr
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```
275 545                 550                 555                 560
278 Glu Ile Tyr Tyr Gln Phe Lys Lys Asp Lys Ala Glu Arg Arg Leu Ala
279                 565                 570                 575
282 Tyr Asn Glu Glu Gln Ile His Lys Phe Asp Lys Gln Lys Leu Tyr Tyr
283             580                 585                 590
286 His Ala Thr Lys Ala Met Thr His Phe Thr Asp Glu Cys Val Lys Lys
287         595                 600                 605
290 Tyr Glu Ala Phe Leu Asn Lys Ser Glu Glu Trp Ile Arg Lys Met Leu
291     610                 615                 620
294 His Leu Arg Lys Gln Leu Leu Ser Leu Thr Asn Gln Cys Phe Asp Ile
295 625                 630                 635                 640
298 Glu Glu Glu Val Ser Lys Tyr Gln Glu Tyr Thr Asn Glu Leu Gln Glu
299                 645                 650                 655
302 Thr Leu Pro Gln Lys Met Phe Thr Ala Ser Ser Gly Ile Lys His Thr
303             660                 665                 670
306 Met Thr Pro Ile Tyr Pro Ser Ser Asn Thr Leu Val Glu Met Thr Leu
307         675                 680                 685
310 Gly Met Lys Lys Leu Lys Glu Glu Met Glu Gly Val Val Lys Glu Leu
311     690                 695                 700
314 Ala Glu Asn Asn His Ile Leu Glu Arg Phe Gly Ser Leu Thr Met Asp
315 705                 710                 715                 720
318 Gly Gly Leu Arg Asn Val Asp Cys Leu
319                 725
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323 <211> LENGTH: 19
324 <212> TYPE: RNA
325 <213> ORGANISM: artificial
327 <220> FEATURE:
328 <223> OTHER INFORMATION: oligonucleotide siTBK-1 sense
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331 ggagacaaca acaagacau                                              19
334 <210> SEQ ID NO: 4
335 <211> LENGTH: 20
336 <212> TYPE: RNA
337 <213> ORGANISM: artificial
339 <220> FEATURE:
340 <223> OTHER INFORMATION: oligonucleotide siTBK-1 antisense
342 <400> SEQUENCE: 4
343 augucuuguu guugucuccc                                            20
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347 <211> LENGTH: 23
348 <212> TYPE: DNA
349 <213> ORGANISM: artificial
351 <220> FEATURE:
352 <223> OTHER INFORMATION: oligonucleotide TBK-1 sense
354 <400> SEQUENCE: 5
355 ttgaagagga gacaacaaca aga                                         23
358 <210> SEQ ID NO: 6
359 <211> LENGTH: 19
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Input Set : A:\50458.002001.txt
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<210> SEQ ID NO: 6
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: artificial
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<210> SEQ ID NO: 7
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: artificial
<220> FEATURE:
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<210> SEQ ID NO: 8
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<210> SEQ ID NO: 9
<211> LENGTH: 20
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/13/2007
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Input Set : **A:\50458.002001.txt**
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10

VERIFICATION SUMMARY DATE: 03/13/2007
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Input Set : **A:\50458.002001.txt**
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